KITTM-A FAM (5'-TCA AAG GAA ACA TGA GTA CCC ACG CTC-3') (SEQ. ID No. 8) and

KITTM-G TET (5'-TCA AAG GAA ACG TGA GTA CCC ACG C-3') (SEQ. ID No. 9)

IN THE CLAIMS:

A marked up version of the claims showing the amendments is attached hereto as Exhibit C. Matter that has been deleted from claims 1, and 3-17 is indicated by brackets and matter that has been added to the claims is indicated by underlining. Please cancel claim 2 without prejudice.

1. A method for determining whether a pig has a white coat color comprising:

(a) obtaining a sample of pig nucleic acid; and

(b) analysing the nucleic acid obtained in (a) to determine whether a mutation is/is not present at an exon 17/intron 17 splice site of *KIT* gene, wherein presence or absence of said mutation is correlated with white coat color.

3. The method according to claim 1, wherein the mutation consists of the substitution of the G of the conserved GT pair for A.

4. The method according to claim 1 or 3, wherein the sample of nucleic acid is amplified prior to analysis.

5. The method according to claim 4, wherein the nucleic acid is genomic DNA.

6. The method according to claim 5, wherein amplification is carried out using PCR and at least one pair of suitable primers.

7. The method according to claim 6, wherein the pair of suitable primers is:
5'-GTA TTC ACA GAG ACT TGG CGG C-3' (SEQ. ID No. 1); and
5'-AAA CCT GCA AGG AAA ATC CTT CAC GG-3' (SEQ. ID No. 2).

8. The method according to claim 5, wherein after amplification the nucleic acid is treated with a restriction enzyme, followed by analysis of fragment lengths.

9. The method according to claim 8, wherein the nucleic acid is treated with the restriction enzyme *Nla*III.

10. The method according to claim 8 or claim 9, wherein the ratio of restriction fragment lengths is determined.

11. The method according to claim 4, wherein the nucleic acid is mRNA.

12. The method according to claim 11, wherein the nucleic acid is amplified using RT-PCR.

13. The method according to claim 12, wherein the length of RT-PCR product is determined.

C16

14. A method for determining whether a pig has a white coat color comprising the step of analysing a sample of pig KIT protein to determine whether the protein is the splice variant protein, said protein being correlated with white coat color.

15. A kit for use in determining whether a pig has a white coat color comprising one or more reagents suitable for determining whether a mutation is present at an exon 17/intron 17 splice site of the *KIT* gene, wherein presence or absence of the mutation is correlated with white coat color.

16. The kit according to claim 15 further comprising one or more reagents for carrying out PCR and one or more pairs of suitable primers.

17. The kit according to claim 16, wherein the pair of suitable primers is:
5'-GTA TTC ACA GAG ACT TGG CGG C-3' (SEQ. ID No. 1); and
5'-AAA CCT GCA AGG AAA ATC CTT CAC GG-3' (SEQ. ID No. 2).

REMARKS

Claims 1 and 3-17, as amended, appear in this application for the Examiner's review and consideration. The amendment to the specification merely includes the SEQ. ID Nos. and does not include any new subject matter. Claims 1 and 3-17 have been amended to more

particularly point out the claimed subject matter and to correct inadvertent minor spelling and editorial errors, but no new matter has been added. Claim 1 has been amended to recite whether a mutation is/is not present at an exon 17/intron 17. The amendment to claim 1 is supported in the specification at p. 5, ll. 4-10 and p. 6, ll. 29-31.

Claims 1, 4, 5, 8, and 10-16 stand rejected under 35 U.S.C. § 112, first paragraph for the reasons set forth on pages 3-5 of the Office Action. Applicants respectfully traverse.

As long as a person of ordinary skill in the art would have understood the inventor to have been in possession of the claimed invention at the time of filing, even if not every nuance of the claims is explicitly described in the specification, then the adequate written description requirement is met. *In re Alton*, 76 F.3d 1168, 37 U.S.P.Q.2d 1578 (Fed. Cir. 1996). "*Ipsis verbis* disclosure is not necessary to satisfy the written description requirement of section 112." *Fujikawa v. Wattanasin*, 93 F.3d 1559, 39 U.S.P.Q.2d 1895 (Fed. Cir. 1996). Moreover, a patent need not teach, and preferably omits, what is well known in the art. *In re Buchner*, 929 F.2d 660, 661, 18 U.S.P.Q.2d 1331, 1332 (Fed. Cir. 1991); *Hybritech, Inc. v. Monoclonal Antibodies, Inc.*, 802 F.2d 1367, 1384, 231 U.S.P.Q. 81, 94 (Fed. Cir. 1986), *cert. denied*, 480 U.S. 947 (1987). Even when experimentation may be required, the fact that experimentation may be complex does not necessarily make it undue, if the art typically engages in such experimentation. *In certain Limited – Charge Cell Culture Microcarriers*, 221 U.S.P.Q. 1165, 1174 (Int'l Trade Comm) 1983), *Aff'd. sub. nom., Massachusetts Institute of Technology v. A.ZB. Fortia*, 774 F.2d 1104, 227 U.S.P.Q. 428 (Fed. Cir. 1985).

The claims as amended now overcome this rejection. The claims have been amended to recite a mutation which is correlated with a white coat color. In particular, the method requires an analysis to determine whether a mutation is/is not present at an exon 17/intron 17 splice site of KIT gene. The specification fully supports this claim scope in particular at pages 5-8, and as shown in table format on page 7. The Office Action requests a list describing a numerical amount of mutations, however, this is unnecessary. The claims contemplate a mutation in the exon 17/intron 17 splice which results in a modified KIT protein with the associated alterations in function and phenotype. A skilled artisan knowing the KIT gene can easily determine whether a mutation has occurred, and whether the mutation is correlated with a white color coat. Thus, the rejection of claims 1, 4, 5, 8, and 10-16 under 35 U.S.C. § 112, first paragraph, cannot stand and should be withdrawn.

Claims 1-17 stand rejected under 35 U.S.C. § 112, first paragraph for the reasons set forth on pages 7-10 of the Office Action. Applicants respectfully traverse.

The test for enablement is whether the experimentation needed to practice the invention is undue or unreasonable. *In re Wands*, 858 F.2d 731, 737, 8 U.S.P.Q.2d 1400, 1404 (Fed. Cir. 1988). A patent need not teach, and preferably omits, what is well known in the art. *In re Buchner*, 929 F.2d 660, 661, 18 U.S.P.Q.2d 1331, 1332 (Fed. Cir. 1991); *Hybritech, Inc. v. Monoclonal Antibodies, Inc.*, 802 F.2d 1367, 1384, 231 U.S.P.Q. 81, 94 (Fed. Cir. 1986), *cert. denied*, 480 U.S. 947 (1987). The fact that experimentation may be complex does not necessarily make it undue, if the art typically engages in such experimentation. *in certain Limited – Charge Cell Culture Microcarriers*, 221 U.S.P.Q. 1165, 1174 (Int'l Trade Comm) 1983), *Aff'd. sub. nom., Massachusetts Institute of Technology v. A.ZB. Fortia*, 774 F.2d 1104, 227 U.S.P.Q. 428 (Fed. Cir. 1985). Nothing more than objective enablement is required, and therefore, it is irrelevant whether the teaching is provided through broad terminology or illustrative examples. *In re Wright*, 000 F.2d 1557, 1561 (Fed. Cir. 1993); *In re Marzocchi*, 439 F.2d 220, 223, 169 U.S.P.Q. 367, 369 (C.C.P.A. 1971).

The claims as amended overcome this rejection. As discussed above, the claims recite a method for determining whether a pig has a white coat color. The method comprises obtaining a sample of pig nucleic acid; and analyzing the nucleic acid obtained in (a) to determine whether a mutation is/is not present at an exon 17/intron 17 splice site of *KIT* gene, wherein presence or absence of said mutation is correlated with white coat color.

The Examiner recognizes that the specification is enabling for a method or kit for determining coat color genotype in a pig. *See*, Office Action page 7. The Office Action, however, unnecessarily limits the claim scope to one mutation. As nothing more than objective enablement is required, Applicants have set forth, including examples, how to determine whether a mutation has occurred. Also, as the *KIT* gene is known, a skilled artisan can easily determine whether a mutation is present at the exon 17/intron 17 splice site of the *KIT* gene. Any necessary experimentation is merely routine and therefore, the patent need not teach, and preferably omits, what is well known in the art.

Thus, the rejection of claims 1-17 under 35 U.S.C. § 112, first paragraph, cannot stand and should be withdrawn.

Claims 1-13 and 15-17 stand rejected under 35 U.S.C. § 112, second paragraph, as allegedly being indefinite for the reasons set forth on page 5 of the Office Action. Claims 1 and 15 have been amended, rendering this rejection moot.

A term in the claims may be given a special meaning in the description of the invention. When the specification states the meaning that a term in the claim is intended to

have, the claim is examined using that meaning, in order to achieve a complete exploration of the applicant's invention and its relation to the prior art. *In re Zletz*, 893 F.2d 319, 13 U.S.P.Q.2d 1320 (Fed. Cir. 1989); MPEP 2173.05(a). Additionally, a claim may not be rejected solely because of the type of language used to define the subject matter for which patent protection is sought. *In re Swinehart*, 439 F.2d 210, 160 U.S.P.Q. 226 (C.C.P.A. 1971), *see also* MPEP 2173.01. The claims should not be rejected for non-inclusion of additional limitations dealing with factors which must be presumed to be within the level of ordinary skill in the art; the claims need not recited such factors where one of ordinary skill in the art to whom the specification and claims are directed would consider them obvious. *See In re Skrivan*, 427 F.2d 801, 806, 166 U.S.P.Q. 85, 88 (C.C.P.A. 1970).

As the claims have been amended to overcome the rejection, the rejection of claims 1-13 and 15-17 under 35 U.S.C. § 112, second paragraph, cannot stand and should be withdrawn.

Claims 15 and 16 stand rejected under 35 U.S.C. 103(a) as rendered obvious over Moller *et al.* Mammalian Genome, *7*, 822-830 (1996) ("Moller") in view of Ahern, "Biochemical Reagent Kits Offer Scientists Good Return on Investment," *The Scientist*, *9*, 1-5 (1995) ("Ahern"), for the reasons set forth on pages 6 and 7 of the Office Action. Applicants respectfully traverse.

The consistent criterion for determination of obviousness is whether the prior art would have suggest to one of ordinary skill in the art that claimed subject matter should be carried out and would have a reasonable likelihood of success. *In re Dow Chemical Co.*, 837 F.2d 469, 473, 5 U.S.P.Q.2d 1529, 1531 (Fed. Cir. 1988). As the Examiner is well aware, in order to form a proper basis for a rejection under 35 U.S.C. § 103, the prior art must provide some suggestion, either explicit or implicit, of the combination that allegedly renders a claimed invention obvious. *M.P.E.P.*, § 2142 (June 1998), *see also, Panduit Corp. v. Denisson Manufacturing Co.*, 1 U.S.P.Q.2d 1593, 1597 (Fed. Cir. 1987). The Examiner can satisfy the burden of showing obviousness of the combination only by showing some objective teaching in the prior art or that knowledge generally available to one of ordinary skill in the art would lead that individual to combine the relevant teachings of the references. *In re Sang Su Lee*, 277 F.3d 1338, 1343, 61 U.S.P.Q.2d 1430 (Fed. Cir. 2002); citing *In re Fritch*, 972 F.2d 1260, 1265, 23 U.S.P.Q.2d 1780, 1783 (Fed. Cir. 1992). The need for specificity is paramount, particular findings must be made as to the reason the skilled artisan, with no knowledge of the claimed invention, would have selected the components for combination in the manner claimed. *Id.* The Examiner's conclusory statements do not

adequately address the issue of motivation to combine; the factual question of motivation is material to patentability, and can not be resolved on subjective belief and unknown authority. *Id.*

The present claims are neither disclosed nor suggested by Moller either alone or in combination with Ahern. The Office Action states that "Moller (1996) teaches primers KIT1F and KIT1R that localize to exon 16 and exon 17 of the KIT gene. Such primers would amplify a fragment contain the intron 16/exon 17 splice site which is encompassed by the recitation of 'exon 17/intron' in the claim." As amended the claims recites exon 17/intron 17, which is neither suggested nor disclosed by Moller either alone or in combination with Ahern. To arrive at the recited claim, however, the Office Action selectively chose two primers from the 14 primers listed on Table 1 with no other guidance than the present claims, *i.e.* the rejection under 35 U.S.C. § 103 is the product of hindsight analysis using the present claims as a blueprint. In fact, Moller teaches against the present claims by focusing the study on *KIT* intron 18. *See*, Moller p. 823 *Cloning and DNA Sequence*, p. 825 last paragraph, p. 826 Figure 3, etc. No motivation exists for the skilled artisan to construct a kit by selecting reagents suitable to determine whether a mutation is present in an exon 17/intron 17 without the aid of the present claims.

To overcome the deficiencies of Moller, the Office Action cites Ahern, however, Ahern provides no further guidance. Ahern generally discusses the use of kits, but does not disclose or suggest the use of the primers in the claims, nor does Ahern suggest selectively choosing from the 14 primers enumerated by Moller.

Accordingly, the rejection of claims 15 and 16 under 35 U.S.C. § 103(a) as rendered obvious by Moller in view of Ahern cannot stand and should be withdrawn.

Accordingly, it is believed that claims 1, 3-17 are now in condition for allowance, early notice of which would be appreciated.

If any outstanding issues remain, the examiner is invited to telephone the undersigned at the telephone number indicated below to discuss the same. No fee is believed to be due for the submission of this response. Should any fees be required, please charge such fees to Brobeck, Phleger & Harrison, LLP Deposit Account No. 50-1640.

Respectfully submitted,

Dated: 7/8/02

By: Craig Puckett
Craig L. Puckett (Reg. No. 43,023)

For:
Laurence Posorske (Reg. No. 34,698)

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EXHIBIT A
REPLACEMENT PARAGRAPH
U.S. PATENT APPLICATION SERIAL NO. 09/550,605

On page 8, lines 20-21:

KIT21 (5'-GTA TTC ACA GAG ACT TGG CGG C-3') (SEQ. ID No. 1); and

KIT35 (5'-AAA CCT GCA AGG AAA ATC CTT CAC GG-3') (SEQ. ID No. 2).

On page 17, paragraph starting at line 21 and ending on page 18, line 12:

ii. RT-PCR of KIT exon 16-19

First strand cDNA synthesis was accomplished using the First-Strand cDNA Synthesis kit (Pharmacia Biotech) so that ~100 ng mRNA was randomly primed by 0.1 μg pd(N6) in a total volume of 15 μl. Two μl of the completed first cDNA strand reaction was then directly used per 12 μl PCR reaction by adding 10 μl PCR mix containing 10 pmol each of the mouse/human derived primers KIT1F and KIT7R (5'-TCR TAC ATA GAA AGA GAY GTG ACT C (SEQ. ID No. 3) and 5'-AGC CTT CCT TGA TCA TCT TGT AG (SEQ. ID No. 4), respectively; Moller *et al.* 1996, *supra*), 1.2 μl 10 x PCR-buffer (10 mM Tris-HCl, pH 8.3, 50 mM KCl) and 0.5 U of AmpliTaq polymerase (Perkin-Elmer) incubated with an equal amount Taqstart antibody (Clonetech) at 25°C for 5 min to achieve a hot start PCR. The reaction was covered with 20 μl mineral oil and thermocycled in a Hybaid Touchdown machine (Hybaid) with 40 cycles at 94°C for 1 min, 55-48°C (touchdown one degree per cycle the first seven cycles and then 48°C in the remaining cycles) for 1 min and 72°C for 1 min. After PCR 2 μl loading dye was added to each sample which were then loaded on 4% agarose gel (Nusieve/Seakem 3:1, FMC Bioproducts) and electrophoresed with 100V for 80 min. Products were visualised by ethidium bromide staining and UV-illumination.

On page 19, paragraph starting on line 24 and ending on page 20, line 9:

i. PCR to produce DNA Sequencing Template

A 175 bp region including the boundary between exon17 and intron17 of the *KIT* gene was amplified for sequence analysis using forward primer KIT21 (5'-GTA TTC ACA GAG ACT TGG CGG C-3') (SEQ. ID No. 1); and reverse primer KIT35 (5'-AAA CCT GCA AGG AAA ATC CTT CAC GG-3') (SEQ. ID No. 2). PCR was carried out on a DNA thermal cycler (Perkin Elmer 9600) in a total volume of 20 μl containing 25 ng genomic DNA, 1.0 mM $MgCl_2$, 50 mM KCl, 10 mM Tris-HCl, pH 8.3, 200 μM dNTPs, 0.5 U AmpliTaq Gold (Perkin Elmer) and 10 pmol of both KIT21 and KIT35 primer. To activate AmpliTaq Gold,

initial heat denaturation was carried out at 94°C, 45 sec at 55°C and 45 sec at 72°C. The final extension lasted for 7 min at 72°C. PCR products were cloned into vector pUC18 using the SureClone ligation kit (Pharmacia Biotech).

On page 29, paragraph at lines 3-14:

The PCR primers used were as described below:

KITTM-Nest-F (5'-CTC CTT ACT CAT GGT CGA ATC ACA-3') (SEQ. ID No. 6) and

KITTM-Nest-R (5'-CGG CTA AAA TGC ATG GTA TGG-3') (SEQ. ID No. 7).

The TaqMan® probes used were:

KITTM-A FAM (5'-TCA AAG GAA ACA TGA GTA CCC ACG CTC-3') (SEQ. ID No. 8) and

KITTM-G TET (5'-TCA AAG GAA ACG TGA GTA CCC ACG C-3') (SEQ. ID No. 9)

EXHIBIT B
MARKED VERSION OF THE REPLACEMENT PARAGRAPH
U.S. PATENT APPLICATION SERIAL NO. 09/550,605

On page 8, lines 20-21:

KIT21 (5'-GTA TTC ACA GAG ACT TGG CGG C-3') (SEQ. ID No. 1); and

KIT35 (5'-AAA CCT GCA AGG AAA ATC CTT CAC GG-3') (SEQ. ID No. 2).

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ii. RT-PCR of KIT exon 16-19

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initial heat denaturation was carried out at 94°C, 45 sec at 55°C and 45 sec at 72°C. The final extension lasted for 7 min at 72°C. PCR products were cloned into vector pUC18 using the SureClone ligation kit (Pharmacia Biotech).

On page 29, paragraph at lines 3-14:

The PCR primers used were as described below:

KITTM-Nest-F (5'-CTC CTT ACT CAT GGT CGA ATC ACA-3') (SEQ. ID No. 6) and

KITTM-Nest-R (5'-CGG CTA AAA TGC ATG GTA TGG-3') (SEQ. ID No. 7).

The TaqMan® probes used were:

KITTM-A FAM (5'-TCA AAG GAA ACA TGA GTA CCC ACG CTC-3') (SEQ. ID No. 8) and

KITTM-G TET (5'-TCA AAG GAA ACG TGA GTA CCC ACG C-3') (SEQ. ID No. 9)

EXHIBIT C
MARKED VERSION OF THE CLAIMS
U.S. PATENT APPLICATION SERIAL NO. 09/550,605

1. (Amended) A method for determining [coat colour genotype in] whether a pig has a white coat color comprising [which comprises]:

(a) obtaining a sample of pig nucleic acid; and

(b) analysing the nucleic acid obtained in (a) to determine whether a mutation is/is not present at an exon 17/intron 17 splice site of *KIT* gene, wherein presence or absence of said mutation is correlated with white coat color.

3. (Amended) [A] The method [is claimed in] according to claim [2] 1, wherein the mutation consists of the substitution of the G of the conserved GT pair for A.

4. (Amended) [A] The method [as claimed in] according to claim 1 or 3, wherein the sample of nucleic acid is amplified prior to analysis.

5. (Amended) [A] The method [as claimed in] according to claim 4, wherein the nucleic acid is genomic DNA.

6. (Amended) [A] The method [as claimed in] according to claim 5, wherein amplification is carried out using PCR and at least one pair of suitable primers.

7. (Amended) [A] The method [as claimed in] according to claim 6, wherein the pair of suitable primers is:

5'-GTA TTC ACA GAG ACT TGG CGG C-3'[)] (SEQ. ID No 1); and

5'-AAA CCT GCA AGG AAA ATC CTT CAC GG-3' (SEQ. ID No. 2).

8. (Amended) [A] The method [as claimed in] according to claim 5, wherein after amplification the nucleic acid is treated with a restriction enzyme, followed by analysis of fragment lengths.

9. (Amended) [A] The method [as claimed in] according to claim 8, wherein the nucleic acid is treated with the restriction enzyme *Nla*III.

10. (Amended) [A] The method [as claimed in] according to claim 8 or claim 9, wherein the ratio of restriction fragment lengths is determined.

11. (Amended) [A] The method [as claimed in] according to claim 4, wherein the nucleic acid is mRNA.

12. (Amended) [A] The method [as claimed in] according to claim 11, wherein the nucleic acid is amplified using RT-PCR.

13. (Amended) [A] The method [as claimed in] according to claim 12, wherein the length of RT-PCR product is determined.

14. (Amended) A method for determining [coat colour genotype in] whether a pig [which comprises] has a white coat color comprising the step of analysing a sample of pig KIT protein to determine whether the protein is the splice variant protein, said protein being correlated with white coat color.

15. (Amended) A kit for use in determining whether [the coat colour genotype of] a pig [which comprises] has a white coat color comprising one or more reagents suitable for determining whether a mutation is present at an exon 17/intron 17 splice site of the *KIT* gene, wherein presence or absence of the mutation is correlated with white coat color.

16. (Amended) [A] The kit [as claimed in] according to claim 15 [which comprises] further comprising one or more reagents for carrying out PCR and one or more pairs of suitable primers.

17. (Amended) [A] The kit [as claimed in] according to claim 16, [which comprises] wherein the [following] pair of suitable primers is:

5'-GTA TTC ACA GAG ACT TGG CGG C-3'[)] (SEQ. ID. No. 1); and

5'-AAA CCT GCA AGG AAA ATC CTT CAC GG-3' (SEQ. ID No. 2).

EXHIBIT D
THE CLAIMS THAT WILL BE PENDING UPON ENTRY OF THE AMENDMENT FILED: July 8, 2002

1. A method for determining whether a pig has a white coat color comprising:

(a) obtaining a sample of pig nucleic acid; and

(b) analysing the nucleic acid obtained in (a) to determine whether a mutation is/is not present at an exon 17/intron 17 splice site of *KIT* gene, wherein presence or absence of said mutation is correlated with white coat color.

2. Canceled.

3. The method according to claim 1, wherein the mutation consists of the substitution of the G of the conserved GT pair for A.

4. The method according to claim 1 or 3, wherein the sample of nucleic acid is amplified prior to analysis.

5. The method according to claim 4, wherein the nucleic acid is genomic DNA.

6. The method according to claim 5, wherein amplification is carried out using PCR and at least one pair of suitable primers.

7. The method according to claim 6, wherein the pair of suitable primers is:
5'-GTA TTC ACA GAG ACT TGG CGG C-3' (SEQ. ID No. 1); and
5'-AAA CCT GCA AGG AAA ATC CTT CAC GG-3' (SEQ. ID No. 2).

8. The method according to claim 5, wherein after amplification the nucleic acid is treated with a restriction enzyme, followed by analysis of fragment lengths.

9. The method according to claim 8, wherein the nucleic acid is treated with the restriction enzyme *Nla*III.

10. The method according to claim 8 or claim 9, wherein the ratio of restriction fragment lengths is determined.

11. The method according to claim 4, wherein the nucleic acid is mRNA.

12. The method according to claim 11, wherein the nucleic acid is amplified using RT-PCR.

13. The method according to claim 12, wherein the length of RT-PCR product is determined.

14. A method for determining whether a pig has a white coat color comprising the step of analysing a sample of pig KIT protein to determine whether the protein is the splice variant protein, said protein being correlated with white coat color.

15. A kit for use in determining whether a pig has a white coat color comprising one or more reagents suitable for determining whether a mutation is present at an exon 17/intron 17 splice site of the *KIT* gene, wherein presence or absence of the mutation is correlated with white coat color.

16. The kit according to claim 15 further comprising one or more reagents for carrying out PCR and one or more pairs of suitable primers.

17. The kit according to claim 16, wherein the pair of suitable primers is:
5'-GTA TTC ACA GAG ACT TGG CGG C-3' (SEQ. ID No. 1); and
5'-AAA CCT GCA AGG AAA ATC CTT CAC GG-3' (SEQ. ID No. 2).